



096429-9141.ST25.txt  
SEQUENCE LISTING

<110> Welch, Rodney A.

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Grys, Thomas E.

<120> E. COLI O157:H7 C1-INH-BINDING PROTEIN AND METHODS OF USE

<130> 096429-9141

<140> Current Application Number: US/10/786,445

<141> 2004-02-25

<150> 10/002,309

<151> 2001-10-26

<150> 60/243,675

<151> 2000-10-26

<160> 25

<170> PatentIn version 3.1

<210> 1

<211> 2798

<212> DNA

<213> Unknown

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<223> Description of Unknown Organism: E. coli O157:H7 plasmid pO157

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<221> CDS

096429-9141.ST25.txt

<222> (138)..(2798)

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 agagatggag aacaccg atg aaa tta aag tat ctg tca tgt acg atc ctt 170  
                   Met Lys Leu Lys Tyr Leu Ser Cys Thr Ile Leu  
                   1                   5                   10  
 gcc cct ctg gcg att ggg gta ttt tct gca aca gct gct gat aat aat 218  
 Ala Pro Leu Ala Ile Gly Val Phe Ser Ala Thr Ala Ala Asp Asn Asn  
                   15                   20                   25  
 tca gcc att tat ttc aat acc tcc cag cct ata aat gat ctg cag ggt 266  
 Ser Ala Ile Tyr Phe Asn Thr Ser Gln Pro Ile Asn Asp Leu Gln Gly  
                   30                   35                   40  
 tcg ttg gcc gca gag gtg aaa ttt gca caa agc cag att tta ccc gcc 314  
 Ser Leu Ala Ala Glu Val Lys Phe Ala Gln Ser Gln Ile Leu Pro Ala  
                   45                   50                   55  
 cat cct aaa gaa ggg gat agt caa cca cat ctg acc agc ctg cgg aaa 362  
 His Pro Lys Glu Gly Asp Ser Gln Pro His Leu Thr Ser Leu Arg Lys  
                   60                   65                   70                   75  
 agt ctg ctg ctt gtc cgt ccg gtg aaa gct gat gat aaa aca cct gtt 410  
 Ser Leu Leu Leu Val Arg Pro Val Lys Ala Asp Asp Lys Thr Pro Val  
                   80                   85                   90  
 cag gtg gaa gcc cgc gat gat aat aat aaa att ctc ggt acg tta acc 458  
 Gln Val Glu Ala Arg Asp Asp Asn Asn Lys Ile Leu Gly Thr Leu Thr  
                   95                   100                   105  
 ctt tat cct cct tca tca cta ccg gat aca atc tac cat ctg gat ggt 506  
 Leu Tyr Pro Pro Ser Ser Leu Pro Asp Thr Ile Tyr His Leu Asp Gly  
                   110                   115                   120  
 gtt ccg gaa ggt ggt atc gat ttc aca cct cat aat gga acg aaa aag 554  
 Val Pro Glu Gly Gly Ile Asp Phe Thr Pro His Asn Gly Thr Lys Lys  
                   125                   130                   135  
 atc att aat acg gtg gct gaa gta aac aaa ctc agt gat gcc agc ggg 602  
 Ile Ile Asn Thr Val Ala Glu Val Asn Lys Leu Ser Asp Ala Ser Gly  
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 Ser Ser Ile His Ser His Leu Thr Asn Asn Ala Leu Val Glu Ile His  
                   160                   165                   170  
 act gca aat ggt cgt tgg gta aga gac att tat ctg ccg cag gga ccc 698  
 Thr Ala Asn Gly Arg Trp Val Arg Asp Ile Tyr Leu Pro Gln Gly Pro  
                   175                   180                   185  
 gac ctt gaa ggt aag atg gtt cgc ttt gtt tcg tct gca ggc tat agt 746  
 Asp Leu Glu Gly Lys Met Val Arg Phe Val Ser Ser Ala Gly Tyr Ser  
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096429-9141.ST25.txt

tca acg gtt ttt tat ggt gat cga aaa gtc aca ctc tcg gtg ggt aac Ser Thr Val Phe Tyr Gly Asp Arg Lys Val Thr Leu Ser Val Gly Asn 205 210 215	794
act ctt ctg ttc aaa tat gta aat ggt cag tgg ttc cgc tcc ggt gaa Thr Leu Leu Phe Lys Tyr Val Asn Gly Gln Trp Phe Arg Ser Gly Glu 220 225 230 235	842
ctg gag aat aat cga atc act tat gct cag cat att tgg agt gct gaa Leu Glu Asn Asn Arg Ile Thr Tyr Ala Gln His Ile Trp Ser Ala Glu 240 245 250	890
ctg cct gcg cac tgg atc gtg cct ggt tta aac ttg gtg att aaa cag Leu Pro Ala His Trp Ile Val Pro Gly Leu Asn Leu Val Ile Lys Gln 255 260 265	938
ggc aat ctg agc ggt cgc cta aat gat atc aag att gga gca ccg ggt Gly Asn Leu Ser Gly Arg Leu Asn Asp Ile Lys Ile Gly Ala Pro Gly 270 275 280	986
gag ctg ttg cat aca att gat atc ggg atg ttg acc act ccc cgg Glu Leu Leu Leu His Thr Ile Asp Ile Gly Met Leu Thr Thr Pro Arg 285 290 295	1034
gat cgc ttt gat ttt gcc aaa gac aaa gaa gca cat agg gaa tat ttc Asp Arg Phe Asp Phe Ala Lys Asp Lys Glu Ala His Arg Glu Tyr Phe 300 305 310 315	1082
cag acc att cct gta agt cgt atg att gtt aat aat tat gcg cct cta Gln Thr Ile Pro Val Ser Arg Met Ile Val Asn Asn Tyr Ala Pro Leu 320 325 330	1130
cac cta aag gaa gtt atg tta cca acc gga gag tta ttg aca gat atg His Leu Lys Glu Val Met Leu Pro Thr Gly Glu Leu Leu Thr Asp Met 335 340 345	1178
gat cca gga aat ggt ggg tgg cat agt ggt aca atg cgt caa aga ata Asp Pro Gly Asn Gly Trp His Ser Gly Thr Met Arg Gln Arg Ile 350 355 360	1226
ggt aaa gaa ttg gtt tcg cat ggc att gat aat gct aac tat ggt tta Gly Lys Glu Leu Val Ser His Gly Ile Asp Asn Ala Asn Tyr Gly Leu 365 370 375	1274
aat agt acc gca ggc tta ggg gag aat agt cat cca tat gta gtt gcg Asn Ser Thr Ala Gly Leu Gly Glu Asn Ser His Pro Tyr Val Val Ala 380 385 390 395	1322
caa tta gcg gca cat aat agc cgc ggt aat tat gct aat ggc atc cag Gln Leu Ala Ala His Asn Ser Arg Gly Asn Tyr Ala Asn Gly Ile Gln 400 405 410	1370
gtt cat ggt ggc tcc gga ggt ggg gga att gtt act tta gat tcc aca Val His Gly Gly Ser Gly Gly Ile Val Thr Leu Asp Ser Thr 415 420 425	1418
ttg ggg aat gag ttc agt cat gaa gtt ggt cat aat tat ggt ctt ggt Leu Gly Asn Glu Phe Ser His Glu Val Gly His Asn Tyr Gly Leu Gly 430 435 440	1466
cat tat gta gat ggt ttc aag ggt tct gta cat cgt agt gca gaa aat His Tyr Val Asp Gly Phe Lys Gly Ser Val His Arg Ser Ala Glu Asn	1514

## 096429-9141.ST25.txt

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460 465 470 475			
aac ttt tat ccg tct caa aca aat gaa aag agt	tgt ctg aat aat cag		1610
Asn Phe Tyr Pro Ser Gln Thr Asn Glu Lys Ser Cys	Leu Asn Asn Gln		
480 485 490			
tgt caa gaa ccg ttt gat gga cac aaa	ttt ggt ttt gac gcc atg gcg		1658
Cys Gln Glu Pro Phe Asp Gly His Lys Phe Gly Phe Asp	Ala Met Ala		
495 500 505			
gga ggc agc cct ttc tct gct gca aac cgt ttc aca	atg tat act ccg		1706
Gly Gly Ser Pro Phe Ser Ala Ala Asn Arg Phe Thr	Met Tyr Thr Pro		
510 515 520			
aat tca tcg gct atc atc cag cgt ttt ttt gaa aat	aaa gct gtg ttc		1754
Asn Ser Ser Ala Ile Ile Gln Arg Phe Phe Glu Asn	Lys Ala Val Phe		
525 530 535			
gat agc cgt tcc tcc acc ggc ttc agc aag tgg aat	gca gat acg cag		1802
Asp Ser Arg Ser Ser Thr Gly Phe Ser Lys Trp Asn Ala	Asp Thr Gln		
540 545 550 555			
gaa atg gaa ccg tat gaa cac acc att gac cgt gcg	gag cag att acg		1850
Glu Met Glu Pro Tyr Glu His Thr Ile Asp Arg Ala	Glu Gln Ile Thr		
560 565 570			
gct tca gtc aat gag cta agt gaa agc aaa atg gct	gag ctg atg gca		1898
Ala Ser Val Asn Glu Leu Ser Glu Ser Lys Met Ala	Glu Leu Met Ala		
575 580 585			
gag tac gct gtc gtc aaa gtg cat atg tgg aac ggt	aac tgg aca aga		1946
Glu Tyr Ala Val Val Lys Val His Met Trp Asn Gly	Asn Trp Thr Arg		
590 595 600			
aac atc tat atc cct aca gcc tcc gca gat aat aga	ggc agt atc ctg		1994
Asn Ile Tyr Ile Pro Thr Ala Ser Ala Asp Asn Arg	Gly Ser Ile Leu		
605 610 615			
acc atc aac cat gag gcc ggt tat aat agt tat ctg	ttt ata aat ggt		2042
Thr Ile Asn His Glu Ala Gly Tyr Asn Ser Tyr Leu	Phe Ile Asn Gly		
620 625 630 635			
gac gaa aag gtc gtt tcc cag ggg tat aaa aag agc	ttt gtt tcc gat		2090
Asp Glu Lys Val Val Ser Gln Gly Tyr Lys Lys Ser	Phe Val Ser Asp		
640 645 650			
ggt cag ttc tgg aaa gaa cgt gat gtg gtt gat act	cgt gaa gcg cgt		2138
Gly Gln Phe Trp Lys Glu Arg Asp Val Val Asp Thr	Arg Glu Ala Arg		
655 660 665			
aag cca gag cag ttt ggt gtt cct gtg acg acc ctg	gtg ggg tat tac		2186
Lys Pro Glu Gln Phe Gly Val Pro Val Thr Thr Leu	Val Gly Tyr Tyr		
670 675 680			
gat ccg gaa ggc acg ctg tca agc tac atc tat cct	gcg atg tat ggt		2234
Asp Pro Glu Gly Thr Leu Ser Ser Tyr Ile Tyr Pro	Ala Met Tyr Gly		
685 690 695			
gcc tat ggc ttc act tat tcc gat gat agt cag aat	cta tcc gat aac		2282

## 096429-9141.ST25.txt

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700					705					710					715			
gac tgc cag ctg cag gtg gat acg aaa gaa ggg cag ttg cga ttc aga															2330			
Asp	Cys	Gln	Leu	Gln	Val	Asp	Thr	Lys	Glu	Gly	Gln	Leu	Arg	Phe	Arg			
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ctg gct aat cac cgg gct aac aac act gta atg aat aag ttc cat att															2378			
Leu	Ala	Asn	His	Arg	Ala	Asn	Asn	Thr	Val	Met	Asn	Lys	Phe	His	Ile			
															735	740	745	
aac gtg cca aca gaa agt cag ccc aca cag gcc aca ttg gtt tgc aat															2426			
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Asn	Lys	Ile	Leu	Asp	Thr	Lys	Ser	Leu	Thr	Pro	Ala	Pro	Glu	Gly	Leu			
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acc tat act gta aat ggg cag gca ctt cca gca aaa gaa aac gag gga															2522			
Thr	Tyr	Thr	Val	Asn	Gly	Gln	Ala	Leu	Pro	Ala	Lys	Glu	Asn	Glu	Gly			
															780	785	790	795
tgc atc gtg tcc gtg aat tca ggt aaa cgt tac tgt ttg ccg gtt ggt															2570			
Cys	Ile	Val	Ser	Val	Asn	Ser	Gly	Lys	Arg	Tyr	Cys	Leu	Pro	Val	Gly			
															800	805	810	
caa cgg tca gga tat agc ctt cct gac tgg att gtt ggg cag gaa gtc															2618			
Gln	Arg	Ser	Gly	Tyr	Ser	Leu	Pro	Asp	Trp	Ile	Val	Gly	Gln	Glu	Val			
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tat gtc gac agc ggg gct aaa gcg aaa gtg ctg ctt tct gac tgg gat															2666			
Tyr	Val	Asp	Ser	Gly	Ala	Lys	Ala	Lys	Val	Leu	Leu	Ser	Asp	Trp	Asp			
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aac ctg tcc tat aac agg att ggt gag ttt gta ggt aat gtg aac cca															2714			
Asn	Leu	Ser	Tyr	Asn	Arg	Ile	Gly	Glu	Phe	Val	Gly	Asn	Val	Asn	Pro			
															845	850	855	
gct gat atg aaa aaa gtt aaa gcc tgg aac gga cag tat ttg gac ttc															2762			
Ala	Asp	Met	Lys	Lys	Val	Lys	Ala	Trp	Asn	Gly	Gln	Tyr	Leu	Asp	Phe			
															860	865	870	875
agt aaa cct agg tca atg agg gtt gta tat aaa taa															2798			
Ser	Lys	Pro	Arg	Ser	Met	Arg	Val	Val	Tyr	Lys								
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&lt;211&gt; 886

&lt;212&gt; PRT

&lt;213&gt; Unknown

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&lt;223&gt; Description of Unknown Organism: E. coli O157:H7 plasmid pO157

&lt;400&gt; 2

096429-9141.ST25.txt

Met Lys Leu Lys Tyr Leu Ser Cys Thr Ile Leu Ala Pro Leu Ala Ile  
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Gly Val Phe Ser Ala Thr Ala Ala Asp Asn Asn Ser Ala Ile Tyr Phe  
20 25 30

Asn Thr Ser Gln Pro Ile Asn Asp Leu Gln Gly Ser Leu Ala Ala Glu  
35 40 45

Val Lys Phe Ala Gln Ser Gln Ile Leu Pro Ala His Pro Lys Glu Gly  
50 55 60

Asp Ser Gln Pro His Leu Thr Ser Leu Arg Lys Ser Leu Leu Leu Val  
65 70 75 80

Arg Pro Val Lys Ala Asp Asp Lys Thr Pro Val Gln Val Glu Ala Arg  
85 90 95

Asp Asp Asn Asn Lys Ile Leu Gly Thr Leu Thr Leu Tyr Pro Pro Ser  
100 105 110

Ser Leu Pro Asp Thr Ile Tyr His Leu Asp Gly Val Pro Glu Gly Gly  
115 120 125

Ile Asp Phe Thr Pro His Asn Gly Thr Lys Lys Ile Ile Asn Thr Val  
130 135 140

Ala Glu Val Asn Lys Leu Ser Asp Ala Ser Gly Ser Ser Ile His Ser  
145 150 155 160

His Leu Thr Asn Asn Ala Leu Val Glu Ile His Thr Ala Asn Gly Arg  
165 170 175

Trp Val Arg Asp Ile Tyr Leu Pro Gln Gly Pro Asp Leu Glu Gly Lys  
180 185 190

Met Val Arg Phe Val Ser Ser Ala Gly Tyr Ser Ser Thr Val Phe Tyr  
195 200 205

Gly Asp Arg Lys Val Thr Leu Ser Val Gly Asn Thr Leu Leu Phe Lys  
210 215 220

Tyr Val Asn Gly Gln Trp Phe Arg Ser Gly Glu Leu Glu Asn Asn Arg  
225 230 235 240

Ile Thr Tyr Ala Gln His Ile Trp Ser Ala Glu Leu Pro Ala His Trp  
245 250 255

096429-9141.ST25.txt

Ile Val Pro Gly Leu Asn Leu Val Ile Lys Gln Gly Asn Leu Ser Gly  
260 265 270

Arg Leu Asn Asp Ile Lys Ile Gly Ala Pro Gly Glu Leu Leu Leu His  
275 280 285

Thr Ile Asp Ile Gly Met Leu Thr Thr Pro Arg Asp Arg Phe Asp Phe  
290 295 300

Ala Lys Asp Lys Glu Ala His Arg Glu Tyr Phe Gln Thr Ile Pro Val  
305 310 315 320

Ser Arg Met Ile Val Asn Asn Tyr Ala Pro Leu His Leu Lys Glu Val  
325 330 335

Met Leu Pro Thr Gly Glu Leu Leu Thr Asp Met Asp Pro Gly Asn Gly  
340 345 350

Gly Trp His Ser Gly Thr Met Arg Gln Arg Ile Gly Lys Glu Leu Val  
355 360 365

Ser His Gly Ile Asp Asn Ala Asn Tyr Gly Leu Asn Ser Thr Ala Gly  
370 375 380

Leu Gly Glu Asn Ser His Pro Tyr Val Val Ala Gln Leu Ala Ala His  
385 390 395 400

Asn Ser Arg Gly Asn Tyr Ala Asn Gly Ile Gln Val His Gly Gly Ser  
405 410 415

Gly Gly Gly Ile Val Thr Leu Asp Ser Thr Leu Gly Asn Glu Phe  
420 425 430

Ser His Glu Val Gly His Asn Tyr Gly Leu Gly His Tyr Val Asp Gly  
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Phe Lys Gly Ser Val His Arg Ser Ala Glu Asn Asn Asn Ser Thr Trp  
450 455 460

Gly Trp Asp Gly Asp Lys Lys Arg Phe Ile Pro Asn Phe Tyr Pro Ser  
465 470 475 480

Gln Thr Asn Glu Lys Ser Cys Leu Asn Asn Gln Cys Gln Glu Pro Phe  
485 490 495

Asp Gly His Lys Phe Gly Phe Asp Ala Met Ala Gly Gly Ser Pro Phe

500

505

510

Ser Ala Ala Asn Arg Phe Thr Met Tyr Thr Pro Asn Ser Ser Ala Ile  
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Ile Gln Arg Phe Phe Glu Asn Lys Ala Val Phe Asp Ser Arg Ser Ser  
 530 535 540

Thr Gly Phe Ser Lys Trp Asn Ala Asp Thr Gln Glu Met Glu Pro Tyr  
 545 550 555 560

Glu His Thr Ile Asp Arg Ala Glu Gln Ile Thr Ala Ser Val Asn Glu  
 565 570 575

Leu Ser Glu Ser Lys Met Ala Glu Leu Met Ala Glu Tyr Ala Val Val  
 580 585 590

Lys Val His Met Trp Asn Gly Asn Trp Thr Arg Asn Ile Tyr Ile Pro  
 595 600 605

Thr Ala Ser Ala Asp Asn Arg Gly Ser Ile Leu Thr Ile Asn His Glu  
 610 615 620

Ala Gly Tyr Asn Ser Tyr Leu Phe Ile Asn Gly Asp Glu Lys Val Val  
 625 630 635 640

Ser Gln Gly Tyr Lys Lys Ser Phe Val Ser Asp Gly Gln Phe Trp Lys  
 645 650 655

Glu Arg Asp Val Val Asp Thr Arg Glu Ala Arg Lys Pro Glu Gln Phe  
 660 665 670

Gly Val Pro Val Thr Thr Leu Val Gly Tyr Tyr Asp Pro Glu Gly Thr  
 675 680 685

Leu Ser Ser Tyr Ile Tyr Pro Ala Met Tyr Gly Ala Tyr Gly Phe Thr  
 690 695 700

Tyr Ser Asp Asp Ser Gln Asn Leu Ser Asp Asn Asp Cys Gln Leu Gln  
 705 710 715 720

Val Asp Thr Lys Glu Gly Gln Leu Arg Phe Arg Leu Ala Asn His Arg  
 725 730 735

Ala Asn Asn Thr Val Met Asn Lys Phe His Ile Asn Val Pro Thr Glu  
 740 745 750

096429-9141.ST25.txt

Ser Gln Pro Thr Gln Ala Thr Leu Val Cys Asn Asn Lys Ile Leu Asp  
755 760 765

Thr Lys Ser Leu Thr Pro Ala Pro Glu Gly Leu Thr Tyr Thr Val Asn  
770 775 780

Gly Gln Ala Leu Pro Ala Lys Glu Asn Glu Gly Cys Ile Val Ser Val  
785 790 795 800

Asn Ser Gly Lys Arg Tyr Cys Leu Pro Val Gly Gln Arg Ser Gly Tyr  
805 810 815

Ser Leu Pro Asp Trp Ile Val Gly Gln Glu Val Tyr Val Asp Ser Gly  
820 825 830

Ala Lys Ala Lys Val Leu Leu Ser Asp Trp Asp Asn Leu Ser Tyr Asn  
835 840 845

Arg Ile Gly Glu Phe Val Gly Asn Val Asn Pro Ala Asp Met Lys Lys  
850 855 860

Val Lys Ala Trp Asn Gly Gln Tyr Leu Asp Phe Ser Lys Pro Arg Ser  
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Met Arg Val Val Tyr Lys  
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<212> PRT

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<223> Description of Unknown Organism: E. coli O157:H7 plasmid pO157

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096429-9141.ST25.txt

<212> DNA

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<212> DNA

<213> Artificial Sequence

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<213> Artificial Sequence

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<223> Synthetic Oligonucleotide

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096429-9141.ST25.txt

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<210> 14

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21

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096429-9141.ST25.txt

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<223> Description of Unknown Organism: *E. coli* 0157:H7 plasmid pO157

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agagatggag aacaccg atg aaa tta aag tat ctg tca tgt acg atc ctt		170
Met Lys Leu Lys Tyr Leu Ser Cys Thr Ile Leu		
1 5 10		
gcc cct ctg gcg att ggg gta ttt tct gca aca gct gct gat aat aat		218
Ala Pro Leu Ala Ile Gly Val Phe Ser Ala Thr Ala Ala Asp Asn Asn		
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tca gcc att tat ttc aat acc tcc cag cct ata aat gat ctg cag ggt		266
Ser Ala Ile Tyr Phe Asn Thr Ser Gln Pro Ile Asn Asp Leu Gln Gly		
30 35 40		
tcg ttg gcc gca gag gtg aaa ttt gca caa agc cag att tta ccc gcc		314
Ser Leu Ala Ala Glu Val Lys Phe Ala Gln Ser Gln Ile Leu Pro Ala		
45 50 55		
cat cct aaa gaa ggg gat agt caa cca cat ctg acc agc ctg cg <sup>g</sup> aaa		362
His Pro Lys Glu Gly Asp Ser Gln Pro His Leu Thr Ser Leu Arg Lys		
60 65 70 75		
agt ctg ctg ctt gtc cgt ccg gtg aaa gct gat gat aaa aca cct gtt		410
Ser Leu Leu Val Arg Pro Val Lys Ala Asp Asp Lys Thr Pro Val		
80 85 90		
cag gtg gaa gcc cgc gat gat aat aat aaa att ctc ggt acg tta acc		458
Gln Val Glu Ala Arg Asp Asp Asn Asn Lys Ile Leu Gly Thr Leu Thr		
95 100 105		
ctt tat cct cct tca tca cta ccg gat aca atc tac cat ctg gat ggt		506
Leu Tyr Pro Pro Ser Ser Leu Pro Asp Thr Ile Tyr His Leu Asp Gly		
110 115 120		
gtt ccg gaa ggt ggt atc gat ttc aca cct cat aat gga acg aaa aag		554
Val Pro Glu Gly Gly Ile Asp Phe Thr Pro His Asn Gly Thr Lys Lys		
125 130 135		
atc att aat acg gtg gct gaa gta aac aaa ctc agt gat gcc agc ggg		602

## 096429-9141.ST25.txt

Ile	Ile	Asn	Thr	Val	Ala	Glu	Val	Asn	Lys	Leu	Ser	Asp	Ala	Ser	Gly	
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Ser	Ser	Ile	His	Ser	His	Leu	Thr	Asn	Asn	Ala	Leu	Val	Glu	Ile	His	
		160						165					170			
act	gca	aat	ggt	cgt	tgg	gta	aga	gac	att	tat	ctg	ccg	cag	gga	ccc	698
Thr	Ala	Asn	Gly	Arg	Trp	Val	Arg	Asp	Ile	Tyr	Leu	Pro	Gln	Gly	Pro	
	175					180			185							
gac	ctt	gaa	ggt	aag	atg	gtt	cgc	ttt	gtt	tcg	tct	gca	ggc	tat	agt	746
Asp	Leu	Glu	Gly	Lys	Met	Val	Arg	Phe	Val	Ser	Ser	Ala	Gly	Tyr	Ser	
	190					195			200							
tca	acg	gtt	ttt	tat	ggt	gat	cga	aaa	gtc	aca	ctc	tcg	gtg	ggt	aac	794
Ser	Thr	Val	Phe	Tyr	Gly	Asp	Arg	Lys	Val	Thr	Leu	Ser	Val	Gly	Asn	
	205					210			215							
act	ctt	ctg	ttc	aaa	tat	gta	aat	ggt	cag	tgg	ttc	cgc	tcc	ggt	gaa	842
Thr	Leu	Leu	Phe	Lys	Tyr	Val	Asn	Gly	Gln	Trp	Phe	Arg	Ser	Gly	Glu	
	220					225			230					235		
ctg	gag	aat	aat	cga	atc	act	tat	gct	cag	cat	att	tgg	agt	gct	gaa	890
Leu	Glu	Asn	Asn	Arg	Ile	Thr	Tyr	Ala	Gln	His	Ile	Trp	Ser	Ala	Glu	
	240					245			250							
ctg	cct	gcg	cac	tgg	atc	gtg	cct	ggt	tta	aac	ttg	gtg	att	aaa	cag	938
Leu	Pro	Ala	His	Trp	Ile	Val	Pro	Gly	Leu	Asn	Leu	Val	Ile	Lys	Gln	
	255					260			265							
ggc	aat	ctg	agc	ggt	cgc	cta	aat	gat	atc	aag	att	gga	gca	ccg	ggt	986
Gly	Asn	Leu	Ser	Gly	Arg	Leu	Asn	Asp	Ile	Lys	Ile	Gly	Ala	Pro	Gly	
	270					275			280							
gag	ctg	ttg	ttg	cat	aca	att	gat	atc	ggg	atg	ttg	acc	act	ccc	cg	1034
Glu	Leu	Leu	Leu	His	Thr	Ile	Asp	Ile	Gly	Met	Leu	Thr	Thr	Pro	Arg	
	285					290			295							
gat	cgc	ttt	gat	ttt	gcc	aaa	gac	aaa	gaa	gca	cat	agg	gaa	tat	ttc	1082
Asp	Arg	Phe	Asp	Phe	Ala	Lys	Asp	Lys	Glu	Ala	His	Arg	Glu	Tyr	Phe	
	300				305				310					315		
cag	acc	att	cct	gta	agt	cgt	atg	att	gtt	aat	aat	tat	gcg	cct	cta	1130
Gln	Thr	Ile	Pro	Val	Ser	Arg	Met	Ile	Val	Asn	Asn	Tyr	Ala	Pro	Leu	
	320					325			330							
cac	cta	aag	gaa	ggt	atg	tta	cca	acc	gga	gag	tta	ttg	aca	gat	atg	1178
His	Leu	Lys	Glu	Val	Met	Leu	Pro	Thr	Gly	Glu	Leu	Leu	Thr	Asp	Met	
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gat	cca	gga	aat	ggt	ggg	tgg	cat	agt	ggt	aca	atg	cgt	caa	aga	ata	1226
Asp	Pro	Gly	Asn	Gly	Gly	Trp	His	Ser	Gly	Thr	Met	Arg	Gln	Arg	Ile	
	350					355				360						
ggt	aaa	gaa	ttg	gtt	tgc	cat	ggc	att	gat	aat	gct	aac	tat	ggt	tta	1274
Gly	Lys	Glu	Leu	Val	Ser	His	Gly	Ile	Asp	Asn	Ala	Asn	Tyr	Gly	Leu	
	365					370				375						
aat	agt	acc	gca	ggc	tta	ggg	gag	aat	agt	cat	cca	tat	gta	gtt	gcf	1322
Asn	Ser	Thr	Ala	Gly	Leu	Gly	Glu	Asn	Ser	His	Pro	Tyr	Val	Val	Ala	
	380					385				390				395		

## 096429-9141.ST25.txt

caa tta gcg gca cat aat agc cgc ggt aat tat gct aat ggc atc cag Gln Leu Ala Ala His Asn Ser Arg Gly Asn Tyr Ala Asn Gly Ile Gln 400 405 410	1370
gtt cat ggt ggc tcc gga ggt ggg gga att gtt act tta gat tcc aca Val His Gly Gly Ser Gly Gly Ile Val Thr Leu Asp Ser Thr 415 420 425	1418
ttg ggg aat gag ttc agt cat gat gtt ggt cat aat tat ggt ctt ggt Leu Gly Asn Glu Phe Ser His Asp Val Gly His Asn Tyr Gly Leu Gly 430 435 440	1466
cat tat gta gat ggt ttc aag ggt tct gta cat cgt agt gca gaa aat His Tyr Val Asp Gly Phe Lys Gly Ser Val His Arg Ser Ala Glu Asn 445 450 455	1514
aac aac tca act tgg gga tgg gat ggt gat aaa aaa cgg ttt att cct Asn Asn Ser Thr Trp Gly Trp Asp Gly Asp Lys Lys Arg Phe Ile Pro 460 465 470 475	1562
aac ttt tat ccg tct caa aca aat gaa aag agt tgt ctg aat aat cag Asn Phe Tyr Pro Ser Gln Thr Asn Glu Lys Ser Cys Leu Asn Asn Gln 480 485 490	1610
tgt caa gaa ccg ttt gat gga cac aaa ttt ggt ttt gac gcc atg gcg Cys Gln Glu Pro Phe Asp Gly His Lys Phe Gly Phe Asp Ala Met Ala 495 500 505	1658
gga ggc agc cct ttc tct gct gca aac cgt ttc aca atg tat act ccg Gly Gly Ser Pro Phe Ser Ala Ala Asn Arg Phe Thr Met Tyr Thr Pro 510 515 520	1706
aat tca tcg gct atc atc cag cgt ttt ttt gaa aat aaa gct gtg ttc Asn Ser Ser Ala Ile Ile Gln Arg Phe Phe Glu Asn Lys Ala Val Phe 525 530 535	1754
gat agc cgt tcc tcc acc ggc ttc agc aag tgg aat gca gat acg cag Asp Ser Arg Ser Ser Thr Gly Phe Ser Lys Trp Asn Ala Asp Thr Gln 540 545 550 555	1802
gaa atg gaa ccg tat gaa cac acc att gac cgt gcg gag cag att acg Glu Met Glu Pro Tyr Glu His Thr Ile Asp Arg Ala Glu Gln Ile Thr 560 565 570	1850
gct tca gtc aat gag cta agt gaa agc aaa atg gct gag ctg atg gca Ala Ser Val Asn Glu Leu Ser Glu Ser Lys Met Ala Glu Leu Met Ala 575 580 585	1898
gag tac gct gtc gtc aaa gtg cat atg tgg aac ggt aac tgg aca aga Glu Tyr Ala Val Val Lys Val His Met Trp Asn Gly Asn Trp Thr Arg 590 595 600	1946
aac atc tat atc cct aca gcc tcc gca gat aat aga ggc agt atc ctg Asn Ile Tyr Ile Pro Thr Ala Ser Ala Asp Asn Arg Gly Ser Ile Leu 605 610 615	1994
acc atc aac cat gag gcc ggt tat aat agt tat ctg ttt ata aat ggt Thr Ile Asn His Glu Ala Gly Tyr Asn Ser Tyr Leu Phe Ile Asn Gly 620 625 630 635	2042
gac gaa aag gtc gtt tcc cag ggg tat aaa aag agc ttt gtt tcc gat Asp Glu Lys Val Val Ser Gln Gly Tyr Lys Lys Ser Phe Val Ser Asp 640 645 650	2090

096429-9141.ST25.txt

ggt cag ttc tgg aaa gaa cgt gat gtg gtt gat act cgt gaa gca gct	2138
Gly Gln Phe Trp Lys Glu Arg Asp Val Val Asp Thr Arg Glu Ala Arg	
655 660 665	
aag cca gag cag ttt ggt gtt cct gtg acg acc ctg gtg ggg tat tac	2186
Lys Pro Glu Gln Phe Gly Val Pro Val Thr Thr Leu Val Gly Tyr Tyr	
670 675 680	
gat ccg gaa ggc acg ctg tca agc tac atc tat cct gca atg tat ggt	2234
Asp Pro Glu Gly Thr Leu Ser Ser Tyr Ile Tyr Pro Ala Met Tyr Gly	
685 690 695	
gcc tat ggc ttc act tat tcc gat gat agt cag aat cta tcc gat aac	2282
Ala Tyr Gly Phe Thr Tyr Ser Asp Asp Ser Gln Asn Leu Ser Asp Asn	
700 705 710 715	
gac tgc cag ctg cag gtg gat acg aaa gaa ggg cag ttg cga ttc aga	2330
Asp Cys Gln Leu Gln Val Asp Thr Lys Glu Gly Gln Leu Arg Phe Arg	
720 725 730	
ctg gct aat cac cgg gct aac aac act gta atg aat aag ttc cat att	2378
Leu Ala Asn His Arg Ala Asn Asn Thr Val Met Asn Lys Phe His Ile	
735 740 745	
aac gtg cca aca gaa agt cag ccc aca cag gcc aca ttg gtt tgc aat	2426
Asn Val Pro Thr Glu Ser Gln Pro Thr Gln Ala Thr Leu Val Cys Asn	
750 755 760	
aac aag ata ctg gat acc aaa tcg ctc aca cct gca cca gaa gga ctt	2474
Asn Lys Ile Leu Asp Thr Lys Ser Leu Thr Pro Ala Pro Glu Gly Leu	
765 770 775	
acc tat act gta aat ggg cag gca ctt cca gca aaa gaa aac gag gga	2522
Thr Tyr Thr Val Asn Gly Gln Ala Leu Pro Ala Lys Glu Asn Glu Gly	
780 785 790 795	
tgc atc gtg tcc gtg aat tca ggt aaa cgt tac tgt ttg ccg gtt ggt	2570
Cys Ile Val Ser Val Asn Ser Gly Lys Arg Tyr Cys Leu Pro Val Gly	
800 805 810	
caa cgg tca gga tat agc ctt cct gac tgg att gtt ggg cag gaa gtc	2618
Gln Arg Ser Gly Tyr Ser Leu Pro Asp Trp Ile Val Gly Gln Glu Val	
815 820 825	
tat gtc gac agc ggg gct aaa gcg aaa gtg ctg ctt tct gac tgg gat	2666
Tyr Val Asp Ser Gly Ala Lys Ala Lys Val Leu Leu Ser Asp Trp Asp	
830 835 840	
aac ctg tcc tat aac agg att ggt gag ttt gta ggt aat gtg aac cca	2714
Asn Leu Ser Tyr Asn Arg Ile Gly Glu Phe Val Gly Asn Val Asn Pro	
845 850 855	
gct gat atg aaa aaa gtt aaa gcc tgg aac gga cag tat ttg gac ttc	2762
Ala Asp Met Lys Lys Val Lys Ala Trp Asn Gly Gln Tyr Leu Asp Phe	
860 865 870 875	
agt aaa cct agg tca atg agg gtt gta tat aaa	2795
Ser Lys Pro Arg Ser Met Arg Val Val Tyr Lys	
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096429-9141.ST25.txt

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Asn Thr Ser Gln Pro Ile Asn Asp Leu Gln Gly Ser Leu Ala Ala Glu  
35 40 45

Val Lys Phe Ala Gln Ser Gln Ile Leu Pro Ala His Pro Lys Glu Gly  
50 55 60

Asp Ser Gln Pro His Leu Thr Ser Leu Arg Lys Ser Leu Leu Leu Val  
65 70 75 80

Arg Pro Val Lys Ala Asp Asp Lys Thr Pro Val Gln Val Glu Ala Arg  
85 90 95

Asp Asp Asn Asn Lys Ile Leu Gly Thr Leu Thr Leu Tyr Pro Pro Ser  
100 105 110

Ser Leu Pro Asp Thr Ile Tyr His Leu Asp Gly Val Pro Glu Gly Gly  
115 120 125

Ile Asp Phe Thr Pro His Asn Gly Thr Lys Lys Ile Ile Asn Thr Val  
130 135 140

Ala Glu Val Asn Lys Leu Ser Asp Ala Ser Gly Ser Ser Ile His Ser  
145 150 155 160

His Leu Thr Asn Asn Ala Leu Val Glu Ile His Thr Ala Asn Gly Arg  
165 170 175

Trp Val Arg Asp Ile Tyr Leu Pro Gln Gly Pro Asp Leu Glu Gly Lys  
180 185 190

## 096429-9141.ST25.txt

Met Val Arg Phe Val Ser Ser Ala Gly Tyr Ser Ser Thr Val Phe Tyr  
 195 200 205

Gly Asp Arg Lys Val Thr Leu Ser Val Gly Asn Thr Leu Leu Phe Lys  
 210 215 220

Tyr Val Asn Gly Gln Trp Phe Arg Ser Gly Glu Leu Glu Asn Asn Arg  
 225 230 235 240

Ile Thr Tyr Ala Gln His Ile Trp Ser Ala Glu Leu Pro Ala His Trp  
 245 250 255

Ile Val Pro Gly Leu Asn Leu Val Ile Lys Gln Gly Asn Leu Ser Gly  
 260 265 270

Arg Leu Asn Asp Ile Lys Ile Gly Ala Pro Gly Glu Leu Leu Leu His  
 275 280 285

Thr Ile Asp Ile Gly Met Leu Thr Thr Pro Arg Asp Arg Phe Asp Phe  
 290 295 300

Ala Lys Asp Lys Glu Ala His Arg Glu Tyr Phe Gln Thr Ile Pro Val  
 305 310 315 320

Ser Arg Met Ile Val Asn Asn Tyr Ala Pro Leu His Leu Lys Glu Val  
 325 330 335

Met Leu Pro Thr Gly Glu Leu Leu Thr Asp Met Asp Pro Gly Asn Gly  
 340 345 350

Gly Trp His Ser Gly Thr Met Arg Gln Arg Ile Gly Lys Glu Leu Val  
 355 360 365

Ser His Gly Ile Asp Asn Ala Asn Tyr Gly Leu Asn Ser Thr Ala Gly  
 370 375 380

Leu Gly Glu Asn Ser His Pro Tyr Val Val Ala Gln Leu Ala Ala His  
 385 390 395 400

Asn Ser Arg Gly Asn Tyr Ala Asn Gly Ile Gln Val His Gly Gly Ser  
 405 410 415

Gly Gly Gly Ile Val Thr Leu Asp Ser Thr Leu Gly Asn Glu Phe  
 420 425 430

Ser His Asp Val Gly His Asn Tyr Gly Leu Gly His Tyr Val Asp Gly  
 435 440 445

096429-9141.ST25.txt

Phe Lys Gly Ser Val His Arg Ser Ala Glu Asn Asn Asn Ser Thr Trp  
450 455 460

Gly Trp Asp Gly Asp Lys Lys Arg Phe Ile Pro Asn Phe Tyr Pro Ser  
465 470 475 480

Gln Thr Asn Glu Lys Ser Cys Leu Asn Asn Gln Cys Gln Glu Pro Phe  
485 490 495

Asp Gly His Lys Phe Gly Phe Asp Ala Met Ala Gly Gly Ser Pro Phe  
500 505 510

Ser Ala Ala Asn Arg Phe Thr Met Tyr Thr Pro Asn Ser Ser Ala Ile  
515 520 525

Ile Gln Arg Phe Phe Glu Asn Lys Ala Val Phe Asp Ser Arg Ser Ser  
530 535 540

Thr Gly Phe Ser Lys Trp Asn Ala Asp Thr Gln Glu Met Glu Pro Tyr  
545 550 555 560

Glu His Thr Ile Asp Arg Ala Glu Gln Ile Thr Ala Ser Val Asn Glu  
565 570 575

Leu Ser Glu Ser Lys Met Ala Glu Leu Met Ala Glu Tyr Ala Val Val  
580 585 590

Lys Val His Met Trp Asn Gly Asn Trp Thr Arg Asn Ile Tyr Ile Pro  
595 600 605

Thr Ala Ser Ala Asp Asn Arg Gly Ser Ile Leu Thr Ile Asn His Glu  
610 615 620

Ala Gly Tyr Asn Ser Tyr Leu Phe Ile Asn Gly Asp Glu Lys Val Val  
625 630 635 640

Ser Gln Gly Tyr Lys Lys Ser Phe Val Ser Asp Gly Gln Phe Trp Lys  
645 650 655

Glu Arg Asp Val Val Asp Thr Arg Glu Ala Arg Lys Pro Glu Gln Phe  
660 665 670

Gly Val Pro Val Thr Thr Leu Val Gly Tyr Tyr Asp Pro Glu Gly Thr  
675 680 685

Leu Ser Ser Tyr Ile Tyr Pro Ala Met Tyr Gly Ala Tyr Gly Phe Thr  
690 695 700

096429-9141.ST25.txt

Tyr Ser Asp Asp Ser Gln Asn Leu Ser Asp Asn Asp Cys Gln Leu Gln  
705 710 715 720

Val Asp Thr Lys Glu Gly Gln Leu Arg Phe Arg Leu Ala Asn His Arg  
725 730 735

Ala Asn Asn Thr Val Met Asn Lys Phe His Ile Asn Val Pro Thr Glu  
740 745 750

Ser Gln Pro Thr Gln Ala Thr Leu Val Cys Asn Asn Lys Ile Leu Asp  
755 760 765

Thr Lys Ser Leu Thr Pro Ala Pro Glu Gly Leu Thr Tyr Thr Val Asn  
770 775 780

Gly Gln Ala Leu Pro Ala Lys Glu Asn Glu Gly Cys Ile Val Ser Val  
785 790 795 800

Asn Ser Gly Lys Arg Tyr Cys Leu Pro Val Gly Gln Arg Ser Gly Tyr  
805 810 815

Ser Leu Pro Asp Trp Ile Val Gly Gln Glu Val Tyr Val Asp Ser Gly  
820 825 830

Ala Lys Ala Lys Val Leu Leu Ser Asp Trp Asp Asn Leu Ser Tyr Asn  
835 840 845

Arg Ile Gly Glu Phe Val Gly Asn Val Asn Pro Ala Asp Met Lys Lys  
850 855 860

Val Lys Ala Trp Asn Gly Gln Tyr Leu Asp Phe Ser Lys Pro Arg Ser  
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Met Arg Val Val Tyr Lys  
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096429-9141.ST25.txt

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096429-9141.ST25.txt

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<223> Synthetic Oligonucleotide

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aaggccccct ctgaggtgtc tgttaaaccc gtgg

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aaaaatggcc acgaagtggc cgcaccgtct cagg

34